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Gene action studies for yield contributing and qualitative characters in Maize (*Zea mays* L.)

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Abstract
The present study was conducted at the research form of STRU, MPKV, Rahuri. An evaluation trial comprising of eight parents, fifty-six F1s (including direct and reciprocal crosses) and two standard checks were conducted during *Rabi* 2018 with three replications in randomized block design. The observation was recorded on three phenological, eleven morphological and four qualitative characters. The estimates of components of SCA variance were higher than the components of GCA variance which indicated preponderance of non-additive gene action for 50 percent Tasseling, days to 50 percent silking, days to maturity, plant height (cm), earhead height (cm), number of nodes per plant, number of leaves per plant, number of ear per plant, number of ear per plot, ear length (cm), ear girth (cm), number of kernel row per ear, number of kernel per ear, 100 kernel weight (g), kernel weight per ear (g), kernel yield per plant (g), kernel yield per plot (kg), kernel yield per hectare (q), protein content (%), starch content (%), tryptophan content (%) and lysine content (%) under present investigation.

Keywords: SCA, GCA, Gene action, Variance

Introduction
Maize (*Zea mays* L.) with chromosome number $2n = 20$ is a new world coarse cereal belonging to the family Gramineae and tribe Maydeae, which includes eight genera. Maize is a crop with a versatile nature. It is grown in more than 166 countries across the globe, including tropical, subtropical and temperate regions, from sea level to 3000 m above sea level. In India, it is cultivated throughout the year in most of its states for various purposes that include grain, feed, fodder, green cobs, sweet corn, baby corn, popcorn, starch and industrial products. It is grown in all three seasons – *Kharif* (rainy), *Rabi* (winter) and *Zaid* (summer).

Worldwide maize is the most imperative cereal crop with the highest global production. It is used as food in humans, feed for poultry and livestock, and raw material for an array of industrial and processed products (Yadav *et al.* 2015) [9]. More than 900 million people depend on maize for their staple food around the world particularly in Latin America, Africa and Asia including India (Shiferaw *et al.* 2011) [9]. Maize provides 62% of the proteins from all cereals in Meso America, while it is 43% in Eastern and Southern Africa, 28% in Andean Region, 22% in West and Central Africa and 4% in South Asia (Hossain *et al.* 2018) [4].

The mating design *viz.,* diallel analysis is commonly used for estimation of genetic variances from single crosses. Knowledge of gene action helps in the selection of parents for use in the hybridization programs and also in the choice of appropriate breeding procedure for the genetic improvement of various quantitative characters.

Material and methods
The experimental material for the present study comprised of eight parental lines is collected from Maize Improvement Project, Kolhapur. All possible crosses n (n-1) were effected during *Kharif* 2018 at the research farm of Seed Technology Research Unit, Mahatma Phule Krishi Vidyapeeth, Rahuri, Dist. Ahmednagar.

The final evaluation trial comprising of eight parents, fifty-six F1s (direct and reciprocal) and two standard checks were conducted during *Rabi* 2018 with three replications in randomized block design at Research farm of Seed Technology Research Unit, Rahuri on a uniform piece of land. All the recommended practices were timely and properly followed to raise a good crop. The observation on days to 50 percent tasseling, days to 50 percent silking and days to maturity were noted on a plot basis. For remaining traits, five competitive plants were randomly selected and tagged at the age of 35 days after sowing in each plot on which observation was recorded from each genotype at different crop growth stages and the average value calculated.

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Results and discussion

The twenty-two characters value of σ²GCA, σ²SCA, σ²A, σ²D, and A: D ratio presented in Table 1. The σ²D component was found higher than the σ²A component in all character *viz.,* days to 50 percent tasseling, days to 50 percent silking, days to maturity, plant height (cm), earhead height (cm), number of nodes per plant, number of leaves per plant, number of ear per plant, number of ear per plot, ear length (cm), ear girth (cm), number of kernel row per ear, number of kernel per ear, 100 kernel weight (g), kernel weight per ear (g), kernel yield per plant (g), kernel yield per plot (kg), kernel yield per hectare (q), protein content (%), starch content (%), tryptophan content (%) and lysine content (%). The SCA variances were also expressed a higher magnitude than the GCA variance.

The ratio of additive to the dominance variance (A:D ratio) indicated that preponderance of non-additive gene action in all characters. The nature of gene action i.e. non-additive observed for all character studied under the present investigation. That could be improved through heterosis breeding and also the production of synthetic and composite variety. The result in consonance with mentioned by Amiruzzaman *et al.* (2011) [1] and Kamble (2012) [5] reported in maize. Bisen *et al.* (2017) [2] for protein content, starch content, tryptophan content and lysine content. Wani *et al.* (2018) [8] showed non-additive gene action for the number of ear per plant. Kumar *et al.* (2019) [6] expressed non-additive gene action for protein content and Tryptophan content. Hassan *et al.* (2019) [3] for days to maturity, plant height, ear length, number of kernel row per ear, number of kernel per ear, 100 kernel weight, number of ear per plant, kernel weight per ear and kernel yield per plant.

Table 1: Analysis of variance of combining ability for different characters in maize

Source	DF	Days to 50 % Tasseling	Days to 50 % Silking	Days to maturity	Plant height (cm)	Earhead height (cm)	Number of nodes per plant	Number of leaves per plant	Number of ears per plant	Number of ears per plot	Ear length (cm)	Ear girth (cm)
GCA	7	66.93**	71.95**	66.97**	906.13**	1693.42**	3.40**	2.88**	0.04**	160.94**	10.52**	7.74 **
SCA	28	12.58**	12.27**	10.99**	460.79**	249.90**	1.03**	0.96**	0.04**	58.88**	5.88**	5.20 **
Reciprocal	28	2.76**	3.013**	3.54**	267.31**	181.66**	0.69**	1.02**	0.05**	40.38**	2.68**	2.27**
Error	126	0.62	0.61	1.05	2.56	2.90	0.10	0.10	0.024	4.13	0.20	0.18
σ² GCA		4.14	4.46	4.12	56.47	105.66	0.21	0.17	0.0013	9.80	0.64	0.47
σ² SCA		11.96	11.66	9.94	458.23	247.00	0.93	0.86	0.017	54.75	5.68	5.03
σ² RCA		1.07	1.20	1.25	132.38	89.38	0.29	0.46	0.011	18.13	1.24	1.05
σ² A		8.29	8.92	8.24	112.95	211.31	0.41	0.35	0.003	19.60	1.29	0.95
σ² D		11.96	11.66	9.94	458.23	247.00	0.93	0.86	0.017	54.75	5.68	5.03
h² % (N.S.)		0.38	0.40	0.40	0.16	0.38	0.24	0.20	0.047	0.20	0.15	0.13
σ² A/ σ² D		0.35	0.38	0.41	0.12	0.43	0.22	0.20	0.075	0.18	0.11	0.10

Cont...

Source	DF	No. of kernel rows per ear	Number of kernel per ear	100 kernel weight (g)	Kernel weight per ear (g)	Kernel yield per plant (g)	Kernel yield per plot (kg)	Kernel yield per (ha)	Protein content (%)	Starch content (%)	Tryptophan content (%)	Lysine content (%)
GCA	7	3.02**	57280.50**	27.28**	3614.93**	5935.92**	9.98**	1819.66**	1.62**	23.48**	0.0011**	0.027**
SCA	28	1.33**	13848.40**	9.44**	779.59**	1429.08**	2.39**	438.58**	1.76**	31.51**	0.0013**	0.035**
Reciprocal	28	1.21**	8171.51**	6.02**	574.48**	768.46**	1.28**	239.24**	1.16**	39.27**	0.0013**	0.11**
Error	126	0.14	34.64	0.53	3.98	3.84	0.02	2.03	0.02	1.84	0.00002	0.0029
σ² GCA		0.18	3577.87	1.67	225.68	370.75	0.62	113.60	0.10	1.35	0.00007	0.0015
σ² SCA		1.19	13813.80	8.91	775.62	1425.23	2.37	436.55	1.74	29.68	0.00126	0.032
σ² RCA		0.54	4068.44	2.74	285.25	382.31	0.63	118.61	0.57	18.72	0.00062	0.053
σ² A		0.36	7155.73	3.34	451.37	741.51	1.24	227.20	0.20	2.71	0.00014	0.0031
σ² D		1.19	13813.80	8.91	775.62	1425.23	2.37	436.55	1.74	29.68	0.00126	0.032
h² % (N.S.)		0.16	0.28	0.21	0.30	0.29	0.29	0.29	0.08	0.05	0.06865	0.034
σ² A/ σ² D		0.15	0.26	0.19	0.29	0.26	0.26	0.26	0.06	0.05	0.05543	0.048

Conclusion

The magnitudes of SCA mean square was found higher than the GCA for all twenty-two characters, which indicated that, the preponderance of non-additive gene action for all characters. Therefore, desirable character improvement could be achieved through the exploitation of heterosis.

Acknowledgment

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